



#G

SEQUENCE LISTING

<110> ~~Felix & Vernet~~ Elma

Vernet, Corine

Shimkets, Richard A.

<120> Novel Human Proteins and Polynucleotides Encoding Them

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<141> 2000-04-06

<150> USSN 60/128,514

<151> 1999-04-09

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<170> PatentIn Ver. 2.0

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Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser
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Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro
100 105 110

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Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro
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Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr
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Cys Ile Phe

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Thr	Met	Gln	Glu	Asp	Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln
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 Cys Leu Phe Gln Gly Val Pro Val Arg Ser Gly Asp Ala Thr Phe Pro
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 Lys Ala Met Asp Asn Val Thr Val Arg Gln Gly Glu Ser Ala Thr Leu
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agg tgc act att gac aac cgg gtc acc cgg gtg gcc tgg cta aac cgc 304
 Arg Cys Thr Ile Asp Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg
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 Ser Thr Ile Leu Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg
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 Asn Val Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr
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 Asp Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser
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ccc aaa att gta gag att tct tca gat atc tcc att aat gaa ggg aac 544
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 140 145 150

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Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro Thr Val
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 Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln Ser Gly Asp Tyr
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gag tgc agt gcc tcc aat gac gtg gcc gcg ccc gtg gta cgg aga gta 736
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 Gly Cys Val Trp Leu Pro Pro Leu Leu Val Leu His Leu Leu Lys
 330 335 340

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Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp Asn Arg Val Thr
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Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp
 65 70 75 80

Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr
 85 90 95

Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro
 100 105 110

Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
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His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
 130 135 140

Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
 145 150 155 160

Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
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Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr
 180 185 190

Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala
 195 200 205

Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
 210 215 220

Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
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Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr
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Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His
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Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr
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Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser
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 Leu Pro Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
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Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp Asn Arg Val Thr
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Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp
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 Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr
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 Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro
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 Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
 115 120 125
 His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
 130 135 140
 Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
 145 150 155 160
 Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
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 Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr
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 Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala
 195 200 205
 Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
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 Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
 225 230 235 240
 Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr
 245 250 255
 Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu
 260 265 270
 Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His
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 Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr
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 Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser
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 Arg Ile Lys Lys Leu Ile Asn Gly Asn Gly Met Pro Val Ala Glu Glu
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 Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser Phe Pro Thr
 70 75 80

cct gag atc cct cat tct ttg gca cca gga aca gtt gca att agt aaa 825
 Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala Ile Ser Lys
 85 90 95

ccc tgg ttc cct gct gtc tca caa atc gca aga gtc caa cgt gtg gat 873
 Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln Arg Val Asp
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 Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser Ser Asn Ala
 135 140 145

acc acc cat gca ggc ata aat aat gaa cat gga tgg ggg agt ctg gag 1017
 Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly Ser Leu Glu
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ctg ctg aat tgaggaagaa agaacacaga aattaaaatt ctcacaaagg 1066
 Leu Leu Asn
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ttaccattaa gctagaggaa gaccacacca ctgtgtgtcc acaaagatac agagccaggc 1126

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Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
 35 40 45

Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Gly Met Pro Val
 50 55 60

Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser
 65 70 75 80

Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
 85 90 95

Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln
 100 105 110

Arg Val Asp Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly
 115 120 125

Lys Ala Thr Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser
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Ser Leu Glu Leu Leu Asn
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 <222> (410)..(889)

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tcgggataac ctgtactgat ttctctgcag gacctttca aagaatcctc ttcaagagag 120
 aaacaaaattt taggctgacg acttcacgga gaggcagggtt ctgctgttgc caatgaacga 180

gaactttcta ctaggctggc ggcatgcaga gcccacgtct gtcagctgcc accttcgtaa 240
 agcacacgtt tcacatgcat gagctcgagt ggctagaact tcaaaaactgt gtcaggttt 300
 ttgttttgg agttataaaa aagttgctca caaacaatag ttattgcctt ttatatcttt 360
 tatgttagtc tactagtcag cattctgccc aaaatggaaa gccactccc atg gga agg 418
 Met Gly Arg
 1

gag ggg gta gca gct ggg agt ctg ctc ttc cag ctg ggg gcc ctc cca 466
 Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly Ala Leu Pro
 5 10 15

ccc cca tgg gga gga aag acg tca agc tcc agc cac tgg ccc cgg tgg 514
 Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser His Trp Pro Arg Trp
 20 25 30 35

gtc cca aag ccc cac ccc tca tgc tct cct ctg gtc acc tct att tac 562
 Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr Ser Ile Tyr
 40 45 50

gct cac atg ccc ctt cct gtc ctt cac ctg cac gtc acc tct att tac 610
 Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr Ser Arg Ser
 55 60 65

cgc caa ccc caa atc tat ctg gtg aaa acc tgg aga aca aca gcg gag 658
 Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr Arg Ala Glu
 70 75 80

tct aag aga gat gta aat gaa aac aca gat caa cag aca cac cag aag 706
 Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr His Gln Lys
 85 90 95

gga agc gtt tcc gcg ggg aaa gga gat gga aag ggg aag aga agt 754
 Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly Lys Arg Ser
 100 105 110 115

gaa gaa ttc tgc gcc cga agc tcg ggt tgg tgt ttg ctc aac tgc ttt 802
 Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu Asn Cys Phe
 120 125 130

act cat ttt aac cct ttc acc tat cct ggg aga aac cca ggc ttg tca 850
 Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro Gly Leu Ser
 135 140 145

cct ttt cat gtt ggg ttg ttt tat tgg cct ctt aag tgagaattga 899

Pro Phe His Val Gly Leu Phe Val Tyr Trp Pro Leu Lys
 150 155 160

tccgtgaagg gaaacagaca ggaggaggc agattgcgaa tacctgggc ttcttagggt 959

ccagtgcggc agttaccgca cctgccttca ccgggtgaacc tttagccagc tgaacaacca 1019

ccaaagcgcc ctgcagagac aagtcatcca gccctctggc atgtccctgg tagccgggc 1079

accagccgct gcggcttgtg aggggcacca tgctccaccc cacggggacc ttcacagttg 1139

aaaaaaagaa gaggaaaaac taattccttc ggtaacagtt tatttcatt tttggaaag 1199

gcaaaaccac tacctggAAC tcgggcctc cgtggtaac ttcttattt tgcttgtat 1259

ttaaaggctg ttctgggtca gggggaaaaa ggtgtctcct tcggtagggatataacg 1319

tggtgataac ctgtcaactg gcagaagcat ccactctgca gggacagtgg cccctcagga 1379

aagcccgccg ctctggcca aggctctc gcagactcca cgggggctca ccctctggcg 1439

tcagggcact ctgaaattcc gacatttctc cttaaagtc tcaacagaca caagagaagt 1499

ttccatcaag caagcactga catattata ttaaaaata gtgaaaatc tcaacattt 1559

tataaataac tctaaacccc tgcttgtaa ttttttctt tacaaggtaa tacacacttt 1619

ctgacttggc actcaaaaat tgccatTTT ttcttctt agttcagaaa acaactttt 1679

tttttaatag gcctttcta ataaaaat actcctgccc tcgcacatac agtttcttt 1739

atcttatata tatTTatata tataatattt cagatctta aacaaaggTT ttgtgcaaAT 1799

atgtctttaa agttaagtga aattatcata aacaaaagaa aataagcatt cacgcacgca 1859

gctcaacttag aaacaagaaa gactactgta gaaatTTTT ttctttgcc ttcaagac 1917

<210> 10

<211> 160

<212> PRT

<213> Homo sapiens

<400> 10

Met Gly Arg Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly

1

5

10

15

Ala Leu Pro Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser His Trp

20

25

30

Pro Arg Trp Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr
 35 40 45

Ser Ile Tyr Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr
 50 55 60

Ser Arg Ser Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr
 65 70 75 80

Arg Ala Glu Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr
 85 90 95

His Gln Lys Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly
 100 105 110

Lys Arg Ser Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu
 115 120 125

Asn Cys Phe Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro
 130 135 140

Gly Leu Ser Pro Phe His Val Gly Leu Phe Val Tyr Trp Pro Leu Lys
 145 150 155 160

<210> 11
 <211> 1279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (410)..(892)

<220>
 <221> misc_feature
 <222> (1225)..(1279)
 <223> where any n may be an a or t or g or c

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tcgggataac ctgtactgat ttctctgcag gacctttca aagaatcctc ttcaagagag 120

aaacaaatcc taggctgacg acttcacgga gaggcaggtt ctgctgttgc caatgaacga 180

gaactttcta ctaggctggc ggcattgcaga gcccacgtct gtcagctgcc accttcgtaa 240

agcacacgtt tcacatgcat gagctcgagt ggctagaact tcaaaaactgt gtcagggttt 300

ttgttttgg a gttataaaa aagttgctca caaacaatag ttattgcctt ttatatcttt 360

tatgttagtc tactagtcag cattctgccc aaaatggaaa gccactccc atg gga agg 418
Met Gly Arg

1

gag ggg gta gca gct ggg agt ctg ctc ttc cag ctg ggg gcc ctc cca 466
Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly Ala Leu Pro

5 10 15

ccc cca tgg gga gga aag acg tca agc tcc agc cac tgg ccc cgg tgg 514
Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser His Trp Pro Arg Trp
20 25 30 35

gtc cca aag ccc cac ccc tca tgc tct cct ctg gtc acc tct att tac 562
Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr Ser Ile Tyr
40 45 50

gct cac atg ccc ctt cct gtc ctt cac ctg cac gtc acc acc agt tcc 610
Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr Ser Arg Ser
55 60 65

cgc caa ccc caa atc tat ctg gtg aaa acc tgg aga aca aca aga gcg gag 658
Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr Arg Ala Glu
70 75 80

tct aag aga gat gta aat gaa aac aca gat caa cag aca cac cag aag 706
Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr His Gln Lys
85 90 95

gga agc gtt gtt tcc gcg ggg aaa gga gat gga aag ggg aag aga agt 754
Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly Lys Arg Ser
100 105 110 115

gaa gaa ttc tgc gcc cga agc tcg ggt tgg tgt ttg ctc aac tgc ttt 802
Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu Asn Cys Phe
120 125 130

act cat ttt aac cct ttc acc tat cct ggg aga aac cca ggc ttg tca 850
Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro Gly Leu Ser
135 140 145

cct ttt cat gtt ggg ttg ttt att ggc ctc tta agt gag aat 892
Pro Phe His Val Gly Leu Phe Ile Gly Leu Leu Ser Glu Asn

150

155

160

tgatccgtga agggaaacag acaggaggag gtcagattgc gaataacctgg ggttcctag 952

ggtccagtgc ggcagttacc gcacctgcct tcaccggtaa accttttagcc agctgaacaa 1012

ccaccaaagc gccctgcaga gacaagtcat cgagccctct ggcattgtccc tggtagcccg 1072

ggcaccagcc gctgcggctt gtgagggca ccatgctcca ccccacgggg accttcacag 1132

ttggaaaaaa gaagagggaaa aactaattcc ttcggtaaca gtttatttcc atttttggga 1192

aaggcaaaac cactacctgg aactcggtgc ctnganntc ttanntnctn nctnagnncnn 1252

atnngnnann nntnnnnnn ncttnna 1279

<210> 12

<211> 161

<212> PRT

<213> Homo sapiens

<400> 12

Met Gly Arg Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly
1 5 10 15Ala Leu Pro Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser Ser His Trp
20 25 30Pro Arg Trp Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr
35 40 45Ser Ile Tyr Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr
50 55 60Ser Arg Ser Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr
65 70 75 80Arg Ala Glu Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr
85 90 95His Gln Lys Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly
100 105 110Lys Arg Ser Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu
115 120 125

Asn Cys Phe Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro

130

135

140

Gly Leu Ser Pro Phe His Val Gly Leu Phe Ile Gly Leu Leu Ser Glu
 145 150 155 160

Asn

<210> 13
 <211> 1689
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (199)..(1146)

<400> 13
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 agctacgtgc ctgtgtgcgg ctctgatggg aggtttatg aaaaccactg taagctccac 120
 cgtgctgctt gcctcctggg aaagaggatc accgtcatcc acagcaagga ctgttcctc 180
 aaaggtgaca cgtgcacc atg gcc ggc tac gcc cgc ttg aag aat gtc ctt 231
 Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu
 1 5 10
 ctg gca ctc cag acc cgt ctg cag cca ctc caa gaa gga gac agc aga 279
 Leu Ala Leu Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg
 15 20 25
 caa gac cct gcc tcc cag aag cgc ctc ctg gtg gaa tct ctg ttc agg 327
 Gln Asp Pro Ala Ser Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg
 30 35 40
 gac tta gat gca gat ggc aat ggc cac ctc agc agc tcc gaa ctg gct 375
 Asp Leu Asp Ala Asp Gly Asn Gly His Leu Ser Ser Glu Leu Ala
 45 50 55
 cag cat gtg ctg aag aag cag gac ctg gat gaa gac tta ctt ggt tgc 423
 Gln His Val Leu Lys Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys
 60 65 70 75
 tca cca ggt gac ctc ctc cga ttt gac gat tac aac agt gac agc tcc 471
 Ser Pro Gly Asp Leu Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser
 80 85 90

ctg acc ctc cgc gag ttc tac atg gcc ttc caa gtg gtt cag ctc agc 519
 Leu Thr Leu Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser
 95 100 105

ctc gcc ccc gag gac agg gtc agt gtg acc aca gtg acc gtg ggg ctg 567
 Leu Ala Pro Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu
 110 115 120

agc aca gtg ctg acc tgc gcc gtc cat gga gac ctg agg cca cca atc 615
 Ser Thr Val Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile
 125 130 135

atc tgg aag cgc aac ggg ctc acc ctg aac ttc ctg gac ttg gaa gac 663
 Ile Trp Lys Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp
 140 145 150 155

atc aat gac ttt gga gag gat tcc ctg tac atc acc aag gtg acc 711
 Ile Asn Asp Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr
 160 165 170

acc atc cac atg ggc aat tac acc tgc cat gct tcc ggc cac gag cag 759
 Thr Ile His Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln
 175 180 185

ctg ttc cag acc cac gtc ctg cag gtg aat gtg ccg cca gtc atc cgt 807
 Leu Phe Gln Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg
 190 195 200

gtc tat cca gag agc cag gca cag gag cct gga gtg gca gcc agc cta 855
 Val Tyr Pro Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu
 205 210 215

aga tgc cat gct gag ggc att ccc atg ccc aga atc act tgg ctg aaa 903
 Arg Cys His Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys
 220 225 230 235

aac ggc gtg gat gtc tca act cag atg tcc aaa cag ctc tcc ctt tta 951
 Asn Gly Val Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu
 240 245 250

gcc aat ggg agc gaa ctc cac atc agc agt gtt cgg tat gaa gac aca 999
 Ala Asn Gly Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr
 255 260 265

ggg gca tac acc tgc att gcc aaa aat gaa gtg ggt gtg gat gaa gat 1047
 Gly Ala Tyr Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp
 270 275 280

atc tcc tcg ctc ttc att gaa gac tca gct aga aag acc ctt gca aac 1095
 Ile Ser Ser Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn
 285 290 295

atc ctg tgg cga gag gaa ggt acc aag ctt cat tgt ttt gcg tca tgc 1143
 Ile Leu Trp Arg Glu Glu Gly Thr Lys Leu His Cys Phe Ala Ser Cys
 300 305 310 315

ctg tgatcacgtg tgtttggttc tatgatgggc cgtcttcca tgatctgcca 1196
 Leu

ccagctttcc cacacaaaagc agccctatgg gagcaggaag tcaatgtcaa attcaagtgg 1256

catatgcatt gaatcaaatt taaaatgtac tcctgtctt aatgagaaat ttttaaatgc 1316

aaagctttca taaaaagtgg cttgtAACCT ctgctgaagc agaacagttg gtaagggttc 1376

ctggtcagat ctgggcctta aactttttc cagtagctga ctgggtttgg gtttagtgtt 1436

ttgcctatct tgtgtggttt taaaaagaca aaacaagttg tagatctcta ctagatagtc 1496

actgtacctt aaatatgctt tgattgagga aaacccgagg aaaaagctgc catgatttct 1556

gccaatgtat attttaaat gtatagatgt ttagaaacat atttatcaag caaatcttta 1616

gtaagttgag ccatatgaag ttgccatTTT tgtgcataa agtggtctaa gattgacaat 1676

ttcatatggc tga 1689

<210> 14
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu Gln Thr
 1 5 10 15

Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro Ala Ser
 20 25 30

Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp Ala Asp
 35 40 45

Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val Leu Lys
 50 55 60

Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu
 65 70 75 80

Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu
 85 90 95

Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro Glu Asp
 100 105 110

Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val Leu Thr
 115 120 125

Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys Arg Asn
 130 135 140

Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp Phe Gly
 145 150 155 160

Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His Met Gly
 165 170 175

Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln Thr His
 180 185 190

Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro Glu Ser
 195 200 205

Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His Ala Glu
 210 215 220

Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val Asp Val
 225 230 235 240

Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly Ser Glu
 245 250 255

Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr Thr Cys
 260 265 270

Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser Leu Phe
 275 280 285

Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp Arg Glu
 290 295 300

Glu Gly Thr Lys Leu His Cys Phe Ala Ser Cys Leu
 305 310 315

<210> 15
 <211> 5573
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (408)..(2933)

<400> 15
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 tggcacatca ttcctcgttt ttggccctcc agctgaacac ctgttctctg tggactgac 120
 tcctcttcc atagggacat catacaacag tcgcctttat ctgagggttgt gcaaagaggg 180
 atggaggaga aaacaatgga gaatccctgg cagattccc caggacgaga gaaggatatc 240
 caattgctca tcagggaaagg tgctaggct cccagccaga cgcctcaga ggccgggtgtc 300
 aagtctccct cacctctgtg atgtgaagtc agctcggtca tgacctggc aggcagaggg 360
 tcagaggggc agatggagca ctcctggcct gatgaagact catcaaa atg aaa cca 416
 Met Lys Pro
 1

gga ggc ttt tgg ctg cat ctc aca ctg ctc gga gcc tcc ctg ccg gct 464
 Gly Gly Phe Trp Leu His Leu Thr Leu Leu Gly Ala Ser Leu Pro Ala
 5 10 15

gcg ctg gga tgg atg gac cca gga acc agc aga ggc ccg gat gtg ggt 512
 Ala Leu Gly Trp Met Asp Pro Gly Thr Ser Arg Gly Pro Asp Val Gly
 20 25 30 35

gtg ggg gag tca cag gca gag gag ccc aga agc ttt gaa gtc aca aga 560
 Val Gly Glu Ser Gln Ala Glu Glu Pro Arg Ser Phe Glu Val Thr Arg
 40 45 50

aga gaa ggg ctt tcc agc cac aac gag ctg ctg gcc tcc tgc ggg aag 608
 Arg Glu Gly Leu Ser Ser His Asn Glu Leu Leu Ala Ser Cys Gly Lys
 55 60 65

aag ttc tgc agc cga ggg agc cgg tgc gtg ctc agc agg aag aca ggg 656
 Lys Phe Cys Ser Arg Gly Ser Arg Cys Val Leu Ser Arg Lys Thr Gly
 70 75 80

gag	ccc	gaa	tgc	cag	tgc	ctg	gag	gca	tgc	agg	ccc	agc	tac	gtg	cct	704
Glu	Pro	Glu	Cys	Gln	Cys	Leu	Glu	Ala	Cys	Arg	Pro	Ser	Tyr	Val	Pro	
85															95	
gtg	tgc	ggc	tct	gat	ggg	agg	ttt	tat	gaa	aac	cac	tgt	aag	ctc	cac	752
Val	Cys	Gly	Ser	Asp	Gly	Arg	Phe	Tyr	Glu	Asn	His	Cys	Lys	Leu	His	
100															115	
cgt	gct	gct	tgc	ctc	ctg	gga	aag	agg	atc	acc	gtc	atc	cac	agc	aag	800
Arg	Ala	Ala	Cys	Leu	Leu	Gly	Lys	Arg	Ile	Thr	Val	Ile	His	Ser	Lys	
120															130	
gac	tgt	ttc	ctc	aaa	ggt	gac	acg	tgc	acc	atg	gcc	gac	tac	gcc	cgc	848
Asp	Cys	Phe	Leu	Lys	Gly	Asp	Thr	Cys	Thr	Met	Ala	Gly	Tyr	Ala	Arg	
135															145	
ttg	aag	aat	gtc	ctt	ctg	gca	ctc	cag	acc	cgt	ctg	cag	cca	ctc	caa	896
Leu	Lys	Asn	Val	Leu	Leu	Ala	Leu	Gln	Thr	Arg	Leu	Gln	Pro	Leu	Gln	
150															160	
gaa	gga	gac	agc	aga	caa	gac	cct	gcc	tcc	cag	aag	cgc	ctc	ctg	gtg	944
Glu	Gly	Asp	Ser	Arg	Gln	Asp	Pro	Ala	Ser	Gln	Lys	Arg	Leu	Leu	Val	
165															175	
gaa	tct	ctg	ttc	agg	gac	tta	gat	gca	gat	ggc	aat	ggc	cac	ctc	agc	992
Glu	Ser	Leu	Phe	Arg	Asp	Leu	Asp	Ala	Asp	Gly	Asn	Gly	His	Leu	Ser	
180															195	
agc	tcc	gaa	ctg	gct	cag	cat	gtg	ctg	aag	aag	cag	gac	ctg	gat	gaa	1040
Ser	Ser	Glù	Leu	Ala	Gln	His	Val	Leu	Lys	Lys	Gln	Asp	Leu	Asp	Glu	
200															210	
gac	tta	ctt	ggt	tgc	tca	cca	ggt	gac	ctc	ctc	cga	ttt	gac	gat	tac	1088
Asp	Leu	Leu	Gly	Cys	Ser	Pro	Gly	Asp	Leu	Leu	Arg	Phe	Asp	Asp	Tyr	
215															225	
aac	agt	gac	agc	tcc	ctg	acc	ctc	cgc	gag	ttc	tac	atg	gcc	ttc	caa	1136
Asn	Ser	Asp	Ser	Ser	Leu	Thr	Leu	Arg	Glu	Phe	Tyr	Met	Ala	Phe	Gln	
230															240	
gtg	gtt	cag	ctc	agc	ctc	gcc	ccc	gag	gac	agg	gtc	agt	gtg	acc	aca	1184
Val	Val	Gln	Leu	Ser	Leu	Ala	Pro	Glu	Asp	Arg	Val	Ser	Val	Thr	Thr	
245															255	
gtg	acc	gtg	ggg	ctg	agc	aca	gtg	ctg	acc	tgc	gcc	gtc	cat	gga	gac	1232
Val	Thr	Val	Gly	Leu	Ser	Thr	Val	Leu	Thr	Cys	Ala	Val	His	Gly	Asp	
260															275	

ctg agg cca cca atc atc tgg aag cgc aac ggg ctc acc acc ctg aac ttc	1280		
Leu Arg Pro Pro Ile Ile Trp Lys Arg Asn Gly Leu Thr Leu Asn Phe			
280	285	290	
ctg gac ttg gaa gac atc aat gac ttt gga gag gat gat tcc ctg tac	1328		
Leu Asp Leu Glu Asp Ile Asn Asp Phe Gly Glu Asp Asp Ser Leu Tyr			
295	300	305	
atc acc aag gtg acc acc atc cac atg ggc aat tac acc tgc cat gct	1376		
Ile Thr Lys Val Thr Thr Ile His Met Gly Asn Tyr Thr Cys His Ala			
310	315	320	
tcc ggc cac gag cag ctg ttc cag acc cac gtc ctg cag gtg aat gtg	1424		
Ser Gly His Glu Gln Leu Phe Gln Thr His Val Leu Gln Val Asn Val			
325	330	335	
ccg cca gtc atc cgt gtc tat cca gag agc cag gca cag gag cct gga	1472		
Pro Pro Val Ile Arg Val Tyr Pro Glu Ser Gln Ala Gln Glu Pro Gly			
340	345	350	355
gtg gca gcc agc cta aga tgc cat gct gag ggc att ccc atg ccc aga	1520		
Val Ala Ala Ser Leu Arg Cys His Ala Glu Gly Ile Pro Met Pro Arg			
360	365	370	
atc act tgg ctg aaa aac ggc gtg gat gtc tca act cag atg tcc aaa	1568		
Ile Thr Trp Leu Lys Asn Gly Val Asp Val Ser Thr Gln Met Ser Lys			
375	380	385	
cag ctc tcc ctt tta gcc aat ggg agc gaa ctc cac atc agc agt gtt	1616		
Gln Leu Ser Leu Leu Ala Asn Gly Ser Glu Leu His Ile Ser Ser Val			
390	395	400	
cggttat gaa gac aca ggg gca tac acc tgc att gcc aaa aat gaa gtg	1664		
Arg Tyr Glu Asp Thr Gly Ala Tyr Thr Cys Ile Ala Lys Asn Glu Val			
405	410	415	
ggt gtg gat gaa gat atc tcc tgc ctc ttc att gaa gac tca gct aga	1712		
Gly Val Asp Glu Asp Ile Ser Ser Leu Phe Ile Glu Asp Ser Ala Arg			
420	425	430	435
aag acc ctt gca aac atc ctg tgg cga gag gaa ggc ctc agc gtg gga	1760		
Lys Thr Leu Ala Asn Ile Leu Trp Arg Glu Glu Gly Leu Ser Val Gly			
440	445	450	
aac atg ttc tat gtc ttc tcc gac gac ggt atc atc gtc atc cat cct	1808		
Asn Met Phe Tyr Val Phe Ser Asp Asp Gly Ile Ile Val Ile His Pro			
455	460	465	

gtg gac tgt gag atc cag agg cac ctc aaa ccc acg gaa aag att ttc 1856
 Val Asp Cys Glu Ile Gln Arg His Leu Lys Pro Thr Glu Lys Ile Phe
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 Met Ser Tyr Glu Glu Ile Cys Pro Gln Arg Glu Lys Asn Ala Thr Gln
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 Pro Cys Gln Trp Val Ser Ala Val Asn Val Arg Asn Arg Tyr Ile Tyr
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cag aaa gtc cta cag tcc ata ggt gtg gac cct ctg ccg gct aag ctg 2048
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 Val His Lys Ser Arg Pro Ser Leu Gln Val Ile Thr Glu Ala Ser Thr
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ccc cag gcc atg gca cac acc cac ctg ggc ggc tac ttc atc cag 2384
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Cys Arg Gln Asp Ser Pro Ala Ser Ala Ala Arg Gln Leu Leu Val Asp	
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680 685 690	
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Pro His Thr Ser Pro Asp Gly Arg Phe Ile Val Ser Ala Ala Asp	
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Ser Pro Trp Leu His Val Gln Glu Ile Thr Val Arg Gly Glu Ile Gln	
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Thr Leu Tyr Asp Leu Gln Ile Asn Ser Gly Ile Ser Asp Leu Ala Phe	
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Gln Arg Ser Phe Thr Glu Ser Asn Gln Tyr Asn Ile Tyr Ala Ala Leu	
740 745 750 755	
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His Thr Glu Pro Asp Leu Leu Phe Leu Glu Leu Ser Thr Gly Lys Val	
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Gly Met Leu Lys Asn Leu Lys Glu Pro Pro Ala Gly Pro Ala Gln Pro	
775 780 785	
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Asp Val Gly Val Gly Glu Ser Gln Ala Glu Glu Pro Arg Ser Phe Glu			
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Val Thr Arg Arg Glu Gly Leu Ser Ser His Asn Glu Leu Leu Ala Ser			
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Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg Cys Val Leu Ser Arg			
65	70	75	80
Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu Ala Cys Arg Pro Ser			
85	90	95	
Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe Tyr Glu Asn His Cys			
100	105	110	
Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys Arg Ile Thr Val Ile			
115	120	125	
His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr Cys Thr Met Ala Gly			
130	135	140	
Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu Gln Thr Arg Leu Gln			
145	150	155	160
Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro Ala Ser Gln Lys Arg			
165	170	175	
Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp Ala Asp Gly Asn Gly			
180	185	190	
His Leu Ser Ser Ser Glu Leu Ala Gln His Val Leu Lys Lys Gln Asp			
195	200	205	
Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu Leu Arg Phe			
210	215	220	
Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu Phe Tyr Met			
225	230	235	240
Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro Glu Asp Arg Val Ser			
245	250	255	
Val Thr Thr Val Thr Val Gly Leu Ser Thr Val Leu Thr Cys Ala Val			

260

265

270

His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys Arg Asn Gly Leu Thr
 275 280 285

Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp Phe Gly Glu Asp Asp
 290 295 300

Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His Met Gly Asn Tyr Thr
 305 310 315 320

Cys His Ala Ser Gly His Glu Gln Leu Phe Gln Thr His Val Leu Gln
 325 330 335

Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro Glu Ser Gln Ala Gln
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Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His Ala Glu Gly Ile Pro
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Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val Asp Val Ser Thr Gln
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Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly Ser Glu Leu His Ile
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Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser Leu Phe Ile Glu Asp
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Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp Arg Glu Glu Gly Leu
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Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp Asp Gly Ile Ile Val
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Ile His Pro Val Asp Cys Glu Ile Gln Arg His Leu Lys Pro Thr Glu
 465 470 475 480

Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro Gln Arg Glu Lys Asn
 485 490 495

Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val Asn Val Arg Asn Arg
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Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg Val Leu Val Val Asp

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Ala Lys Leu Ser Tyr Asp Lys Ser His Asp Gln Val Trp Val Leu Ser		
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Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu Gln Val Ile Thr Glu		
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Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg Thr Pro Phe Ala Gly		
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Val Asp Asp Phe Phe Ile Pro Pro Thr Asn Leu Ile Ile Asn His Ile		
595	600	605
Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro Ala Val His Lys Val		
610	615	620
Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile Gly Leu His His His		
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Gly Cys Val Pro Gln Ala Met Ala His Thr His Leu Gly Gly Tyr Phe		
645	650	655
Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser Ala Ala Arg Gln Leu		
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Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly Pro Asn Gly Asp Val		
675	680	685
Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg Phe Ile Val Ser Ala		
690	695	700
Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu Ile Thr Val Arg Gly		
705	710	715
Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn Ser Gly Ile Ser Asp		
725	730	735
Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn Gln Tyr Asn Ile Tyr		
740	745	750
Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe Leu Glu Leu Ser Thr		
755	760	765
Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu Pro Pro Ala Gly Pro		

770

775

780

Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met Arg Asp Ser Gly Leu
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Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu Ser Leu Phe Leu Ile
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atg cag tgt gat gtt ggt gat gga cgc ctg ttt cgc ctt tca ctt aaa 467

Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys

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10

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cgt gcc ctt tcc agc tgc cct gac ctc ttt ggg ctt tcc agc cgc aac 515

Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn

20

25

30

gag ctg ctg gcc tcc tgc ggg aag aag ttc tgc agc cga ggg agc cgg 563

Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg
 35 40 45

tgc gtg ctc agc agg aag aca ggg gag ccc gaa tgc cag tgc ctg gag 611
 Cys Val Leu Ser Arg Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu
 50 55 60

gca tgc agg ccc agc tac gtg cct gtg tgc ggc tct gat ggg agg ttt 659
 Ala Cys Arg Pro Ser Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe
 65 70 75 80

tat gaa aac cac tgt aag ctc cac cgt gct gct tgc ctc ctg gga aag 707
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 85 90 95

agg atc acc gtc atc cac agc aag gac tgt ttc ctc aaa ggt gac acg 755
 Arg Ile Thr Val Ile His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr
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tgc acc atg gcc ggc tac gcc cgc ttg aag aat gtc ctt ctg gca ctc 803
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 115 120 125

cag acc cgt ctg cag cca ctc caa gaa gga gac agc aga caa gac cct 851
 Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro
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 145 150 155 160

gca gat ggc aat ggc cac ctc agc agc tcc gaa ctg gct cag cat gtg 947
 Ala Asp Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val
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ctg aag aag cag gac ctg gat gaa gac tta ctt ggt tgc tca cca ggt 995
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 180 185 190

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 Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro
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Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val			
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Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys			
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Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln			
290	295	300	
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Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro			
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gag agc cag gca cag gag cct gga gtg gca gcc agc cta aga tgc cat			1427
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Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser			
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ctc ttc att gaa gac tca gct aga aag acc ctt gca aac atc ctg tgg			1667
Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp			
405	410	415	
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Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp			
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Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His			
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Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro			
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Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val			
465	470	475	480
aat gtc cgg aac cgg tac atc tat gtg gcc cag cca gca ctg agc aga			1907
Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg			
485	490	495	
gtc ctt gtg gtc gac atc caa gcc cag aaa gtc cta cag tcc ata ggt			1955
Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly			
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Val Trp Val Leu Ser Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu			
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Gln Val Ile Thr Glu Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg			
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aca ccc ttt gca gga gtg gat gat ttc ttc att ccc cca aca aac ctc			2147
Thr Pro Phe Ala Gly Val Asp Asp Phe Phe Ile Pro Pro Thr Asn Leu			
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Ile Ile Asn His Ile Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro			
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Ala Val His Lys Val Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile			
595	600	605	
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gct gcc cga cag ctg ctc gtt gac agt gtc aca gac tct gtg ctt ggc 2387
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 645 650 655

ccc aat ggt gat gta aca ggc acc cca cac aca tcc ccc gac ggg cgc 2435
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 660 665 670

ttc ata gtc agt gct gca gct gac agc ccc tgg ctg cac gtg cag gag 2483
 Phe Ile Val Ser Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu
 675 680 685

atc aca gtg cgg ggc gag atc cag acc ctg tat gac ctg caa ata aac 2531
 Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn
 690 695 700

tcg ggc atc tca gac ttg gcc ttc cag cgc tcc ttc act gaa agc aat 2579
 Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn
 705 710 715 720

caa tac aac atc tac gcg gct ctg cac acg gag ccg gac ctg ctg ttc 2627
 Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe
 725 730 735

ctg gag ctg tcc acg ggg aag gtg ggc atg ctg aag aac tta aag gag 2675
 Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu
 740 745 750

cca ccc gca ggg cca gct cag ccc tgg ggg ggt acc cac aga atc atg 2723
 Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met
 755 760 765

agg gac agt ggg ctg ttt gga cag tac ctc ctc aca cca gcc cga gag 2771
 Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu
 770 775 780

tca ctg ttc ctc atc aat ggg aga caa aac acg ctg cgg tgt gag gtg 2819
 Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val
 785 790 795 800

tca ggt ata aag ggg ggg acc aca gtg gtg tgg gtg ggt gag gta 2864

Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val
 805 810 815

tgaaggccc agagcagagc cctggccaa ggaacacccc ctagtctga cactgcagcc 2924
 tcaagcaggt acgctgtaca ttttacaga caaaagcaaa aacctgtact cgcttgcgg 2984
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 ggtttttcg ttaggaagta tgatttatgc cttgagctac gatgagaaca tatgctgctg 3104
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 actactgcat ttcctttagt tgtctcaggc tgtggtgact ctcacatggg catcgaagaa 4124
 gtacaacccca catgccttc tggagaccgc ctagatcaga gactcagcaa aaacaggctc 4184
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gcaagccaca cgggttggga gaggtggtct caccacagac gtcttgcta atttggccac 4304
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 cgaagcagggc ctgaaggcata ggtcagggtt tcaggagttc agccccagga ggcaaagtca 5144
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 catacttcac cccagcagag gttcatggga cacagttgga aagccactgg gaggaaatgc 5324
 ctcactacag gggggcctcc ttagcaagc ccagccggta atcctctaa tgaacccaca 5384
 aggtcaattc acaactgata tcttagctat taaagaagta ctgactttac caaaagaatc 5444
 atcaagaaag ctattnatataa aaaaaaaaaaatt aattnaac 5502

<210> 18
 <211> 815
 <212> PRT
 <213> Homo sapiens

<400> 18

Met	Gln	Cys	Asp	Val	Gly	Asp	Gly	Arg	Leu	Phe	Arg	Leu	Ser	Leu	Lys
1				5				10					15		

Arg	Ala	Leu	Ser	Ser	Cys	Pro	Asp	Leu	Phe	Gly	Leu	Ser	Ser	Arg	Asn
							20		25				30		

Glu	Leu	Leu	Ala	Ser	Cys	Gly	Lys	Lys	Phe	Cys	Ser	Arg	Gly	Ser	Arg
						35		40			45				

Cys	Val	Leu	Ser	Arg	Lys	Thr	Gly	Glu	Pro	Glu	Cys	Gln	Cys	Leu	Glu
						50		55			60				

Ala	Cys	Arg	Pro	Ser	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asp	Gly	Arg	Phe
						65		70			75		80		

Tyr	Glu	Asn	His	Cys	Lys	Leu	His	Arg	Ala	Ala	Cys	Leu	Leu	Gly	Lys
						85		90			95				

Arg	Ile	Thr	Val	Ile	His	Ser	Lys	Asp	Cys	Phe	Leu	Lys	Gly	Asp	Thr
							100		105		110				

Cys	Thr	Met	Ala	Gly	Tyr	Ala	Arg	Leu	Lys	Asn	Val	Leu	Leu	Ala	Leu
							115		120		125				

Gln	Thr	Arg	Leu	Gln	Pro	Leu	Gln	Glu	Gly	Asp	Ser	Arg	Gln	Asp	Pro
						130		135		140					

Ala	Ser	Gln	Lys	Arg	Leu	Leu	Val	Glu	Ser	Leu	Phe	Arg	Asp	Leu	Asp
						145		150		155		160			

Ala	Asp	Gly	Asn	Gly	His	Leu	Ser	Ser	Ser	Glu	Leu	Ala	Gln	His	Val
						165		170		175					

Leu	Lys	Lys	Gln	Asp	Leu	Asp	Glu	Asp	Leu	Leu	Gly	Cys	Ser	Pro	Gly
						180		185		190					

Asp	Leu	Leu	Arg	Phe	Asp	Asp	Tyr	Asn	Ser	Asp	Ser	Ser	Leu	Thr	Leu
							195		200		205				

Arg	Glu	Phe	Tyr	Met	Ala	Phe	Gln	Val	Val	Gln	Leu	Ser	Leu	Ala	Pro
							210		215		220				

Glu	Asp	Arg	Val	Ser	Val	Thr	Thr	Val	Thr	Val	Gly	Leu	Ser	Thr	Val
						225		230		235		240			

Leu	Thr	Cys	Ala	Val	His	Gly	Asp	Leu	Arg	Pro	Pro	Ile	Ile	Trp	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245

250

255

Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp
 260 265 270

Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His
 275 280 285

Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln
 290 295 300

Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro
 305 310 315 320

Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His
 325 330 335

Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val
 340 345 350

Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly
 355 360 365

Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr
 370 375 380

Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser
 385 390 395 400

Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp
 405 410 415

Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp
 420 425 430

Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His
 435 440 445

Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro
 450 455 460

Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val
 465 470 475 480

Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg
 485 490 495

Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly

500	505	510
Val Asp Pro Leu Pro Ala Lys Leu Ser Tyr Asp Lys Ser His Asp Gln		
515	520	525
Val Trp Val Leu Ser Trp Gly Asp Val His Lys Ser Arg Pro Ser Leu		
530	535	540
Gln Val Ile Thr Glu Ala Ser Thr Gly Gln Ser Gln His Leu Ile Arg		
545	550	555
Thr Pro Phe Ala Gly Val Asp Asp Phe Phe Ile Pro Pro Thr Asn Leu		
565	570	575
Ile Ile Asn His Ile Arg Phe Gly Phe Ile Phe Asn Lys Ser Asp Pro		
580	585	590
Ala Val His Lys Val Asp Leu Glu Thr Met Met Pro Leu Lys Thr Ile		
595	600	605
Gly Leu His His His Gly Cys Val Pro Gln Ala Met Ala His Thr His		
610	615	620
Leu Gly Gly Tyr Phe Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser		
625	630	635
640		
Ala Ala Arg Gln Leu Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly		
645	650	655
Pro Asn Gly Asp Val Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg		
660	665	670
Phe Ile Val Ser Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu		
675	680	685
Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn		
690	695	700
Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn		
705	710	715
720		
Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe		
725	730	735
Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu		
740	745	750
Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met		

755

760

765

Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu
 770 775 780

Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val
 785 790 795 800

Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val
 805 810 815

<210> 19

<211> 1208

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (124)..(1089)

<400> 19

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gtggcttaat ccgtctccac caccagatct ttctccgtgg attcctctgc taagaccgct 120

gcc atg cca gtg acg gta acc cgc acc acc atc aca acc acc acg acg 168
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
 1 5 10 15

tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg tcc cct cgg gcc 216
 Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala
 20 25 30

ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag ctg gtg tct acc 264
 Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr
 35 40 45

tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc tgg acg ggg tcc 312
 Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser
 50 55 60

atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc tcc gtg acc 360
 Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr
 65 70 75

ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag gcc cgc ttc ccc 408
 Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro

80

— 85

90

95

ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc tat gcg gcc ctc 456
 Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu
 100 105 110

ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc tat gtc cag ttc 504
 Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe
 115 120 125

ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc gcc acc ttc ttc 552
 Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe
 130 135 140

tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg gcc tgg acc cgg 600
 Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg
 145 150 155

gcc cgg ccc ggc gag atc act ggc tat atg gcc acc gta ccc ggg ctg 648
 Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu
 160 165 170 175

ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc ttc gcg ttc atc 696
 Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile
 180 185 190

agc gac ccc aac ctg tac cag cac cag ccg gcc ctg gag tgg tgc gtg 744
 Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val
 195 200 205

gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc gtc atc ctg 792
 Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu
 210 215 220

aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc ttc ccc agc ttc 840
 Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe
 225 230 235

ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat gcc acc gcc ctt 888
 Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
 240 245 250 255

gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat ggc ggc cag cct 936
 Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro
 260 265 270

cgg cgc tcg aga gat gta agc tgc agc cgc agc cat gcc tac tac gtg 984
 Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val

275

280

285

tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg acg gcc atc aac 1032
 Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn
 290 295 300

cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc cac ctg gtt ttt 1080
 Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe
 305 310 315

gtc aag gtc taagactctc ccaagaggct cccgttccct ctccaaacctc 1129
 Val Lys Val
 320

tttgttcttc ttgcccaggt tttctttatg gagtacttct ttccctccgccc tttccctctgt 1189
 ttccctcttc ctgtctccc 1208

<210> 20
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Ser
 1 5 10 15

Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala Leu
 20 25 30

Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
 35 40 45

Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
 50 55 60

Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
 65 70 75 80

Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu
 85 90 95

Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu Phe
 100 105 110

Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu
 115 120 125

<210> 21
<211> 1203
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS

<222> (587)..(1012)

<400> 21

ggaagaagaa ggaggaggag gagaaggaga agaagaagga gaagaacgca agacttcgtc 60

tcaaaaaaaaaa agaagaaaaa atttaatac atttaaaaaa gaaggttgca tgctgtggag 120

caaccagaca attgtgatga aatgtgaagc acaaggcacc agctgtgacg tgttttgcc 180

aagaagtcaa accacgttcc aactaaacct ctagagcaaa ctttcatttt cagcaaattc 240

gaagaaaaga ggaataatgt aaatgacccc acaggaaac agacaaaccc tgaatgtgga 300

gcatttcaca ggacaaaacc tggacagaca tcgaaacact tacaggatgt gtgtagtgtg 360

gcatgacaga gaacttttgtt ttccttaat gtgactgttag acctggcagt gttactataa 420

gaatcactgg caatcagaca cccgggtgtg ctgagctggc actcagtgaa ggccggctact 480

gctcatgtga ttgtggagta gacagttgga agaagtaccc agtccatgg gagagttaaa 540

actgtgccta acagaggtgt cctctgactt ttcttcgtca agctcc atg ttt tca 595

Met Phe Ser

1

cat ctt ccc ttt gac tgt gtc ctg ctg ctg cta cta ctt aca 643
His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu Leu Thr
5 10 15agg tcc tca gaa gtg gaa tac aga gcg gag gtc ggt cag aat gcc tat 691
Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr
20 25 30 35ctg ccc tgc ttc tac acc cca gcc ccc ggg aac ctc gtg ccc gtc 739
Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val
40 45 50tgc tgg ggc aaa gga gcc tgt cct gtg ttt gaa tgt ggc aac gtg gtg 787
Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val
55 60 65ctc agg act gat gaa agg gat gtg aat tat tgg aca tcc aga tac tgg 835
Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp
70 75 80cta aat ggg gat ttc cgc aaa gga gat gtg tcc ctg acc ata gag aat 883
Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr Ile Glu Asn
85 90 95

gtg act cta gca gac agt ggg atc tac tgc tgc cgg atc caa atc cca 931
 Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro
 100 105 110 115

ggc ata atg aat gat gaa aaa ttt aac ctg aag ttg gtc atc aaa cca 979
 Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro
 120 125 130

ggt gag tgg aca ttt gca tgc cat ctt tat gaa taagattat ctgtggatca 1032
 Gly Glu Trp Thr Phe Ala Cys His Leu Tyr Glu
 135 140

tattaaaggt actgattgtt ctcatctctg acttccctaa ttatagccct ggaggagggc 1092

cactaagacc taaagttaa caggccccat tggtgatgct cagtgatatt taacacctc 1152

tctctgtttt aaaactcatg ggtgtgcctg ggcgtggtgg ctcacacctc t 1203

<210> 22
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 22
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 1 5 10 15

Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
 20 25 30

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
 35 40 45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
 50 55 60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
 65 70 75 80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
 85 90 95

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
 100 105 110

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val

115

120

125

Ile Lys Pro Gly Glu Trp Thr Phe Ala Cys His Leu Tyr Glu
 130 135 140

<210> 23
 <211> 825
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (494) .. (769)

<400> 23
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 ccggggccagt tgttctggat ttgtctgatt gcttctccct gtttggagtc aggtggaaca 120
 gctctggcag gaacgcccccc ccgggcaatg cagagtccctc ctccaggagg cacttagtgt 180
 ccatgcgtca ctttgctggat gatgcttcac tggatcaattt gtttccgggg ttgtccgcac 240
 gtctccctgt agtgcaggtg ctccattccctc tttccaattt gcctgtggga tgggacttgg 300
 aagctgtgtc tgttctgctc cactggcaac ctttttttca atgacttaag ctgggttttt 360
 gccatttcc atactctatc atggggagtg ttcaatgtc gcatcttagag atctccctg 420
 gccccatcac agctagagct atgctgtccc ctttcaggaa catcttgtaa tttatccacc 480
 cagcccccaa ctg atg gac ata aag gct gtc tcc cca tca tct cct gct 529
 Met Asp Ile Lys Ala Val Ser Pro Ser Ser Pro Ala
 1 5 10
 act aca gac agc act gca ggg act gtc ctg ctg tgt ttt ttt aag gca 577
 Thr Thr Asp Ser Thr Ala Gly Thr Val Leu Leu Cys Phe Phe Lys Ala
 15 20 25
 tgg gta ctc cag aag cag ttg ctc agc tgc acc ccc aag gtt gag tgg 625
 Trp Val Leu Gln Lys Gln Leu Leu Ser Cys Thr Pro Lys Val Glu Trp
 30 35 40
 aag tcc ctc ggt aaa gga gga gga gag agt gtg aag gga atg gca agg 673
 Lys Ser Leu Gly Lys Gly Gly Glu Ser Val Lys Gly Met Ala Arg
 45 50 55 60

cgg gga ggg aga cag ggc aca ggt gtc ctg gca aca gca gat ggg aaa 721
 Arg Gly Gly Arg Gln Gly Thr Gly Val Leu Ala Thr Ala Asp Gly Lys
 65 70 75

cag gtc tgg cta agg tac cag aag cca aca agt ccc aga aag gtc aag 769
 Gln Val Trp Leu Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys
 80 85 90

tgactttccc aaggtcacac agcaagttga tggcagagct gggtagacca ctcaga 825

<210> 24
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Asp Ile Lys Ala Val Ser Pro Ser Ser Pro Ala Thr Thr Asp Ser
 1 5 10 15

Thr Ala Gly Thr Val Leu Leu Cys Phe Phe Lys Ala Trp Val Leu Gln
 20 25 30

Lys Gln Leu Leu Ser Cys Thr Pro Lys Val Glu Trp Lys Ser Leu Gly
 35 40 45

Lys Gly Gly Glu Ser Val Lys Gly Met Ala Arg Arg Gly Gly Arg
 50 55 60

Gln Gly Thr Gly Val Leu Ala Thr Ala Asp Gly Lys Gln Val Trp Leu
 65 70 75 80

Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys
 85 90

<210> 25
 <211> 1099
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (83) .. (889)

<400> 25
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tctctctgag agccagggcc ac atg gct cac ctg gtg aac tcc gtc agc gac	112		
Met Ala His Leu Val Asn Ser Val Ser Asp			
1	5	10	
atc ctg gat gcc ctg cag agg gac cgg ggg ctg ggc cgg ccc cgc aac	160		
Ile Leu Asp Ala Leu Gln Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn			
15	20	25	
aag gcc gac ctt cag aga gcg cct gcc cgg gga acc cgg ccc cgg ggc	208		
Lys Ala Asp Leu Gln Arg Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly			
30	35	40	
tgt gcc act ggc tcc cgg ccc cga gac tgt ctg gac gtc ctc cta agc	256		
Cys Ala Thr Gly Ser Arg Pro Arg Asp Cys Leu Asp Val Leu Leu Ser			
45	50	55	
gga cag cag gac gat ggc gtc tac tct gtc ttt ccc acc cac tac ccg	304		
Gly Gln Gln Asp Asp Gly Val Tyr Ser Val Phe Pro Thr His Tyr Pro			
60	65	70	
gcc ggc ttc cag gtg tac tgt gac atg cgc acg gac ggc ggc ggc tgg	352		
Ala Gly Phe Gln Val Tyr Cys Asp Met Arg Thr Asp Gly Gly Trp			
75	80	85	90
acg gtg ttt cag cgc cgg gag gac ggc tcc gtg aac ttc ttc cgg ggc	400		
Thr Val Phe Gln Arg Arg Glu Asp Gly Ser Val Asn Phe Phe Arg Gly			
95	100	105	
tgg gat gcg tac cga gac ggc ttt ggc agg ctc acc ggg gag cac tgg	448		
Trp Asp Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr Gly Glu His Trp			
110	115	120	
cta ggg ctc aag agg atc cac gcc ctg acc aca cag gct gcc tac gag	496		
Leu Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln Ala Ala Tyr Glu			
125	130	135	
ctg cac gtg gac ctg gag gac ttt gag aat ggc acg gcc tat gcc cgc	544		
Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr Ala Tyr Ala Arg			
140	145	150	
tac ggg agc ttc ggc gtg ggc ttg ttc tcc gtg gac cct gag gaa gac	592		
Tyr Gly Ser Phe Gly Val Gly Leu Phe Ser Val Asp Pro Glu Glu Asp			
155	160	165	170
ggg tac ccg ctc acc gtg gct gac tat tcc ggc act gca ggc gac tcc	640		
Gly Tyr Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr Ala Gly Asp Ser			
175	180	185	

ctc ctg aag cac agc ggc atg agg ttc acc acc aag gac cgt gac agc 688
 Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys Asp Arg Asp Ser
 190 195 200

gac cat tca gag aac aac tgt gcc gcc ttc tac cgc ggt gcc tgg tgg 736
 Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp
 205 210 215

tac cgc aac tgc cac acg tcc aac ctc aat ggg cag tac ctg cgc ggt 784
 Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly
 220 225 230

gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc tcc tgg acc ggc 832
 Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser Ser Trp Thr Gly
 235 240 245 250

tgg cag tac tca ctc aag ttc tct gag atg aag atc cgg ccg gtc cgg 880
 Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile Arg Pro Val Arg
 255 260 265

gag gac cgc tagaccggtg caccttgtcc ttggccctgc tggccctgt 929
 Glu Asp Arg

cgcggccatcc ccgaccccac ctcactcttt cgtgaatgtt ctccacccac ctgtgcctgg 989

cggacccact ctccagtagg gagggggccgg gccatccctg acacgaagct ccctggccg 1049

gtgaagtcac acatcgccctt ctcggcgtcc ccacccctc catttggcag 1099

<210> 26

<211> 269

<212> PRT

<213> Homo sapiens

<400> 26

Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln
 1 5 10 15

Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg
 20 25 30

Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg
 35 40 45

Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp Gly
 50 55 60

Val Tyr Ser Val Phe Pro Thr His Tyr Pro Ala Gly Phe Gln Val Tyr
 65 70 75 80

 Cys Asp Met Arg Thr Asp Gly Gly Trp Thr Val Phe Gln Arg Arg
 85 90 95

 Glu Asp Gly Ser Val Asn Phe Phe Arg Gly Trp Asp Ala Tyr Arg Asp
 100 105 110

 Gly Phe Gly Arg Leu Thr Gly Glu His Trp Leu Gly Leu Lys Arg Ile
 115 120 125

 His Ala Leu Thr Thr Gln Ala Ala Tyr Glu Leu His Val Asp Leu Glu
 130 135 140

 Asp Phe Glu Asn Gly Thr Ala Tyr Ala Arg Tyr Gly Ser Phe Gly Val
 145 150 155 160

 Gly Leu Phe Ser Val Asp Pro Glu Glu Asp Gly Tyr Pro Leu Thr Val
 165 170 175

 Ala Asp Tyr Ser Gly Thr Ala Gly Asp Ser Leu Leu Lys His Ser Gly
 180 185 190

 Met Arg Phe Thr Thr Lys Asp Arg Asp Ser Asp His Ser Glu Asn Asn
 195 200 205

 Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp Tyr Arg Asn Cys His Thr
 210 215 220

 Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala
 225 230 235 240

 Asp Gly Val Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys
 245 250 255

 Phe Ser Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
 260 265

<210> 27
 <211> 1054
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (38) .. (844)

<400> 27

ccgcctcatc cagttctct ctgagagcca gggccac atg gct cac ctg gtg aac 55
 Met Ala His Leu Val Asn
 1 5

tcc gtc agc gac atc ctg gat gcc ctg cag agg gac cgg ggg ctg ggc 103
 Ser Val Ser Asp Ile Leu Asp Ala Leu Gln Arg Asp Arg Gly Leu Gly
 10 15 20

cgg ccc cgc aac aag gcc gac ctt cag aga gcg cct gcc cgg gga acc 151
 Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg Ala Pro Ala Arg Gly Thr
 25 30 35

cgg ccc cgg ggc tgt gcc act ggc tcc cgg ccc cga gac tgt ctg gac 199
 Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg Pro Arg Asp Cys Leu Asp
 40 45 50

gtc ctc cta agc gga cag cag gac gat ggc gtc tac tct gtc ttt ccc 247
 Val Leu Leu Ser Gly Gln Gln Asp Asp Gly Val Tyr Ser Val Phe Pro
 55 60 65 70

acc cac tac ccg gcc ggc ttc cag gtg tac tgt gac atg cgc acg gac 295
 Thr His Tyr Pro Ala Gly Phe Gln Val Tyr Cys Asp Met Arg Thr Asp
 75 80 85

ggc ggc ggc tgg acg gtg ttt cag cgc cgg gag gac ggc tcc gtg aac 343
 Gly Gly Gly Trp Thr Val Phe Gln Arg Arg Glu Asp Gly Ser Val Asn
 90 95 100

ttc ttc cgg ggc tgg gat gcg tac cga gac ggc ttt ggc agg ctc acc 391
 Phe Phe Arg Gly Trp Asp Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr
 105 110 115

ggg gag cac tgg cta ggg ctc aag agg atc cac gcc ctg acc aca cag 439
 Gly Glu His Trp Leu Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln
 120 125 130

gct gcc tac gag ctg cac gtg gac ctg gag gac ttt gag aat ggc acg 487
 Ala Ala Tyr Glu Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr
 135 140 145 150

gcc tat gcc cgc tac ggg agc ttc ggc gtg ggc ttg ttc gcc gtg gac 535
 Ala Tyr Ala Arg Tyr Gly Ser Phe Gly Val Gly Leu Phe Ala Val Asp
 155 160 165

cct gag gaa gac ggg cac ccc ctc acc gtg gct gac tat tcc ggc act 583
 Pro Glu Glu Asp Gly His Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr

170

175

180

gca ggc gac tcc ctc ctg aag cac agc ggc atg agg ttc acc acc aag 631
 Ala Gly Asp Ser Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys
 185 190 195

gac cgt gac agc gac cat tca gag aac aac tgt gcc gcc ttc tac cgc 679
 Asp Arg Asp Ser Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg
 200 205 210

ggg gcc tgg tgg tac cgc aac tgc cac acg tcc aac ctc aat ggg cag 727
 Gly Ala Trp Trp Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln
 215 220 225 230

tac ctg cgc ggt gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc 775
 Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser
 235 240 245

tcc tgg acc ggc tgg cag tac tca ctc aag ttc tct gag atg aag atc 823
 Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile
 250 255 260

cgg ccg gtc cgg gag gac cgc tagaccggtg caccttgc ttggccctgc 874
 Arg Pro Val Arg Glu Asp Arg
 265

tggtccctgt cgccccatcc ccgaccccac ctcactctt cgtaatgtt ctccacccac 934

ctgtgcctgg cggacccact ctccagtagg gaggggcccgg gccatccctg acacgaagct 994

ccctgggcccgg gtgaagtcac acatcgccctt ctcgcgtcc ccaccccttc catttggcag 1054

<210> 28

<211> 269

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln
 1 5 10 15

Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg
 20 25 30

Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg
 35 40 45

Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp Gly
 50 55 60

Val Tyr Ser Val Phe Pro Thr His Tyr Pro Ala Gly Phe Gln Val Tyr
 65 70 75 80

Cys Asp Met Arg Thr Asp Gly Gly Trp Thr Val Phe Gln Arg Arg
 85 90 95

Glu Asp Gly Ser Val Asn Phe Phe Arg Gly Trp Asp Ala Tyr Arg Asp
 100 105 110

Gly Phe Gly Arg Leu Thr Gly Glu His Trp Leu Gly Leu Lys Arg Ile
 115 120 125

His Ala Leu Thr Thr Gln Ala Ala Tyr Glu Leu His Val Asp Leu Glu
 130 135 140

Asp Phe Glu Asn Gly Thr Ala Tyr Ala Arg Tyr Gly Ser Phe Gly Val
 145 150 155 160

Gly Leu Phe Ala Val Asp Pro Glu Glu Asp Gly His Pro Leu Thr Val
 165 170 175

Ala Asp Tyr Ser Gly Thr Ala Gly Asp Ser Leu Leu Lys His Ser Gly
 180 185 190

Met Arg Phe Thr Thr Lys Asp Arg Asp Ser Asp His Ser Glu Asn Asn
 195 200 205

Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp Tyr Arg Asn Cys His Thr
 210 215 220

Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala
 225 230 235 240

Asp Gly Val Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys
 245 250 255

Phe Ser Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
 260 265

<210> 29
 <211> 498
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(498)

<400> 29

atg aat ttt ctg aaa tta att gct gtg ttt ata gtt ttt agc cat gca 48
 Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
 1 5 10 15

tcg gaa tca cct cag gac tcc act ccc aat caa tta tat atc tgg ggg 96
 Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
 20 25 30

agg acc aag gcg ttg gta ttt ttc aga agc tcc act ggt gat tct gac 144
 Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
 35 40 45

agc aca gct agg att aag aaa ctg atc aat ggg aac agc atg cct gtt 192
 Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
 50 55 60

gca gag gag ctt ccc tgg gaa atg tca cac aca gaa cat caa tct tcc 240
 Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser
 65 70 75 80

ttc ccc act cct gag atc cct cat tct ttg gca cca gga aca gtt gca 288
 Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
 85 90 95

att agt aaa ccc tgg ttc cct gct gtc tca caa atc gca aga gtc caa 336
 Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln
 100 105 110

cgt gtg gat ata aac ttt tgt tca tgg gag gat ctt tct ccc agt gga 384
 Arg Val Asp Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly
 115 120 125

aaa gca act ggg aaa agc agg aca cac tgc aca gtg act gca gtt tca 432
 Lys Ala Thr Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser
 130 135 140

tcc aat gcc acc acc cat gca ggc ata aat aat gaa cat gga tgg ggg 480
 Ser Asn Ala Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly
 145 150 155 160

agt ctg gag ctg ctg aat 498
 Ser Leu Glu Leu Leu Asn
 165

<210> 30
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 30

Met	Asn	Phe	Leu	Lys	Leu	Ile	Ala	Val	Phe	Ile	Val	Phe	Ser	His	Ala
1															15

Ser	Glu	Ser	Pro	Gln	Asp	Ser	Thr	Pro	Asn	Gln	Leu	Tyr	Ile	Trp	Gly
															30

Arg	Thr	Lys	Ala	Leu	Val	Phe	Phe	Arg	Ser	Ser	Thr	Gly	Asp	Ser	Asp
															45

Ser	Thr	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Asn	Gly	Asn	Ser	Met	Pro	Val
															60

Ala	Glu	Glu	Leu	Pro	Trp	Glu	Met	Ser	His	Thr	Glu	His	Gln	Ser	Ser
															80

Phe	Pro	Thr	Pro	Glu	Ile	Pro	His	Ser	Leu	Ala	Pro	Gly	Thr	Val	Ala
															95

Ile	Ser	Lys	Pro	Trp	Phe	Pro	Ala	Val	Ser	Gln	Ile	Ala	Arg	Val	Gln
															110

Arg	Val	Asp	Ile	Asn	Phe	Cys	Ser	Trp	Glu	Asp	Leu	Ser	Pro	Ser	Gly
															125

Lys	Ala	Thr	Gly	Lys	Ser	Arg	Thr	His	Cys	Thr	Val	Thr	Ala	Val	Ser
															140

Ser	Asn	Ala	Thr	Thr	His	Ala	Gly	Ile	Asn	Asn	Glu	His	Gly	Trp	Gly
															160

Ser	Leu	Glu	Leu	Leu	Asn										
															165

<210> 31
 <211> 717
 <212> DNA
 <213> Homo sapiens

<400> 31

cagagagcgc ctgcccgggg aaccggggcc cggggatgtg caactggctc cggccccga 60
 gactgtctgg acgtcctcct aagcgacag caggacatg gctactc tgtctttccc 120
 acccaactacc cggccggctt ccaggtgtac tgtgacatgc gcacggacgg cggccggctgg 180
 acggtgttcc agcgccggga ggacggctcc gtgaacttct tccggggctg ggacgcgtac 240
 cgagacggct ttggcaggct caccggggag cactggctag ggctcaagag gatccacgccc 300
 ctgaccacac aggctgccta cgagctgcac gtggacctgg aggactttga gaatggcacg 360
 gcctatgccc gctacgggag cttcggcgtg ggcttgcgtg ccgtggaccc tgaggaagac 420
 gggtacccgc tcaccgtggc tgactattcc ggcactgcag gcgactccct cctgaagcac 480
 agcgccatga ggttcaccac caaggaccgt gacagcgacc attcagagaa caactgtgcc 540
 gccttctacc gcggtgcctg gtggtaccgc aactgccaca cgtccaaacct caatggcag 600
 tacctgcgcg gtgcgcacgc ctctatgcc gacggcgtgg agtggtcctc ctggaccggc 660
 tggcagtact cactcaagtt ctctgagatg aagatccggc cggtccggga ggaccgc 717

<210> 32
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 32
 ctcgtcctcg agggtaagcc tatccctaac 30

<210> 33
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 33
 ctcgtcgggc ccctgatcag cgggtttaaa c 31

<210> 34
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 34
ctcgtagat ctcgcagcgg agatgccacc ttcccaaag 40

<210> 35
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 35
ctcgccctcg agcctccctcg acgtgccgtt gtcacacctcg 40

<210> 36
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 36
ggatccacca tgaattttct gaaattaatt gctgtgttta tag 43

<210> 37
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 37
ctcgagattc agcagctcca gactccccca tccatg 36

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 38
agatctcaga gagcgccctgc ccggggaaacc

30

<210> 39
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 39
ctcgaggcgg tcctcccgga ccggccggat c

31

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 40
gaggacggct ccgtgaac

18

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 41
gttcacggag ccgtcctc

18

<210> 42
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 42
cagcggcatg aggttcacc

19

<210> 43
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 43
ggtgaacctc atgccgctg

19

<210> 44
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 44
catggtcagc ctac

14

<210> 45
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 45
tcgagtaggc tgac

14

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 46
tccctggaa atgtcacaca 20

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 47
ttcctggtgc caaagaatga g 21

<210> 48
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 48
agaacatcaa ttttccttcc ccactcctga .g 31

<210> 49
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 49
gcctggctct ctggatagac a 21

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 50
cacgagcagc tgttccagac

20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 51
tggcggcaca ttcacctgca g

21

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 52
aaaggcggag gaaagaagta ctc

23

<210> 53
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 53
gctcccggttc cctctcca

18

<210> 54
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 54
cctcttggtt cttcttgccc gagtttctt t 31

<210> 55
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 55
tggaagtccc tcggtaaagg a 21

<210> 56
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 56
aggacacaccc tgccctgtct 20

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 57
cccgcccttgc cattcccttc a 21